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Rabinowitz, Joshua D.
Schweizer, Johannes
Arbor Vita Corporation

<120> Molecular Interactions in Hematopoietic
Cells

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Gly Tyr Ile Ala
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Asn Gly Tyr Ile Ala
1          5

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Thr Asn Gly Tyr Ile Ala
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1          5

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Leu Leu Gln Thr Leu Leu
1          5

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Val Leu Leu Gln Thr Leu Leu
1          5

    <210> 128
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1          5

    <210> 129
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Pro Pro Ile Asp Leu
1          5

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Ser Pro Pro Ile Asp Leu
1          5

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Ser Tyr Thr Met Ile
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    <210> 139
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Glu His Ser Val Ile
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1          5

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1          5

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Ala Asp Thr Glu Leu
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1          5

    <210> 154
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Arg Val Ala Leu Ile
1          5

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Ala Arg Val Ala Leu Ile
1          5

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Val Leu Ala Arg Val Ala Leu Ile
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Ser Ser Met Ala
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Thr Ser Ser Met Ala
1          5

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Ser Thr Ser Ser Met Ala
1          5

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Pro Cys Ser Thr Ser Ser Met Ala
1          5

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Lys Ser Lys Val
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Gln Lys Ser Lys Val
1           5

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Ala Gln Lys Ser Lys Val
1           5

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Glu Ala Gln Lys Ser Lys Val
1           5

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    <220>
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Val Glu Ala Gln Lys Ser Lys Val
1           5

    <210> 168
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    <220>
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    <210> 169
    <211> 5
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Pro Ser Tyr Ile Leu
1           5

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Lys Pro Ser Tyr Ile Leu
1           5

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Gln Lys Pro Ser Tyr Ile Leu
1           5

    <210> 172
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    <400> 172
Tyr Gln Lys Pro Ser Tyr Ile Leu
1           5

    <210> 173
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    <220>
    <223> Tat peptide

    <400> 173
Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly
1           5           10

    <210> 174
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<220>
<223> Tat-CD3 carboxyl terminus fusion peptide

<400> 174
Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Pro Pro Ser
 1          5          10          15
Ser Ser Ser Gly Leu
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<210> 175
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<220>
<223> PDZ ligand

<400> 175
Ser Ala Glu Val
1

<210> 176
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<220>
<223> Tat-CLASP2 carboxyl terminus fusion peptide

<400> 176
Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Met Thr Ser
 1          5          10          15
Ser Ser Ser Val Val
          20

<210> 177
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<220>
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<400> 177
Thr Glu Leu Val
1

<210> 178
<211> 5
<212> PRT
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<220>
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<400> 178
Lys Thr Glu Leu Val
1          5

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<210> 179
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<220>
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<400> 179
His Lys Thr Glu Leu Val
1 5

<210> 180
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<220>
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<400> 180
Pro His Lys Thr Glu Leu Val
1 5

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<400> 181
Thr Pro His Lys Thr Glu Leu Val
1 5

<210> 182
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Ser Ala Gln Val
1

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<400> 183
Ser Ser Ala Gln Val
1 5

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Ser Ser Ser Ala Gln Val
1          5

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Ile Ser Ser Ser Ala Gln Val
1          5

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Ser Ile Ser Ser Ser Ala Gln Val
1          5

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Ser Ser Val Val
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    <220>
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    <400> 188
Ser Ser Ser Val Val
1          5

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<210> 189
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<220>
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<400> 189
Ser Ser Ser Ser Val Val
1 5

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Thr Ser Ser Ser Ser Val Val
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Met Thr Ser Ser Ser Ser Val Val
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Tyr Ala Glu Val
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Arg Tyr Ala Glu Val
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Pro Arg Tyr Ala Glu Val
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Ser Pro Arg Tyr Ala Glu Val
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Gly Ser Pro Arg Tyr Ala Glu Val
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Lys Ser Lys Val
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Gln Lys Ser Lys Val
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    <400> 203
Ile Phe Thr Asp Val
1          5

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Lys Ile Phe Thr Asp Val
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Lys Lys Ile Phe Thr Asp Val
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Ile Lys Lys Ile Phe Thr Asp Val
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    <400> 208
Leu Ser Thr Asp Leu
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Ser Leu Ser Thr Asp Leu
1           5

      <210> 210
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      <210> 211
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      <210> 212
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      <220>
      <223> HPV66 carboxy terminus

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Glu Ser Thr Val
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      <210> 213
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Lys Glu Phe Tyr Ala
1           5

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Thr Lys Glu Phe Tyr Ala
1           5

    <210> 215
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    <400> 215
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1           5

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    <400> 217
Leu Thr Thr Phe
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    <400> 218
Ser Leu Thr Thr Phe
1           5

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 Thr Ser Leu Thr Thr Phe
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 Ala Thr Ser Leu Thr Thr Phe
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 Cys Ser Thr Ser Ser Met Ala
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 Glu Ser Asp Val
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1          5

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Met Pro Ser Ile Glu Ser Asp Val
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Glu Tyr Tyr Val
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Asp Lys Glu Tyr Tyr Val
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Lys Asp Lys Glu Tyr Tyr Val
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Asn Lys Asp Lys Glu Tyr Tyr Val
 1             5

    <210> 233
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    <220>
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    <400> 233
Glu Tyr Phe Ile
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<210> 234
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Lys Glu Tyr Phe Ile
1 5

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Arg Lys Glu Tyr Phe Ile
1 5

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Ser Arg Lys Glu Tyr Phe Ile
1 5

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<400> 237
Ser Ser Arg Lys Glu Tyr Phe Ile
1 5

<210> 238
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ motif

<400> 238
Lys Thr Ile Ala
1

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<210> 239
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ motif

<400> 239
Gly Lys Thr Ile Ala
1          5

<210> 240
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ motif

<400> 240
Phe Gly Lys Thr Ile Ala
1          5

<210> 241
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ motif

<400> 241
Thr Phe Gly Lys Thr Ile Ala
1          5

<210> 242
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ motif

<400> 242
Thr Thr Phe Gly Lys Thr Ile Ala
1          5

<210> 243
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Tat-CLASP1 carboxyl terminus fusion peptide

<400> 243
Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Ser Ile Ser
1          5          10          15
Ser Ser Ala Glu Val
          20

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    <210> 244
    <211> 4
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 244
Val Ser Phe Val
1

    <210> 245
    <211> 5
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 245
Leu Val Ser Phe Val
1          5

    <210> 246
    <211> 6
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 246
Ser Leu Val Ser Phe Val
1          5

    <210> 247
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 247
Gln Ser Leu Val Ser Phe Val
1          5

    <210> 248
    <211> 8
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 248
Gly Gln Ser Leu Val Ser Phe Val
1          5

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<210> 249
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ ligand

<400> 249
Thr Thr Arg Val
1

<210> 250
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ ligand

<400> 250
Glu Thr Glu Val
1

<210> 251
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ ligand

<400> 251
Ala Gln Arg Leu
1

<210> 252
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ ligand

<400> 252
His Asp Ala Leu
1

<210> 253
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> PDZ motif

<400> 253
Ile Thr Arg Leu
1

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    <210> 254
    <211> 5
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 254
Asp Ile Thr Arg Leu
 1           5

    <210> 255
    <211> 6
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 255
Arg Asp Ile Thr Arg Leu
 1           5

    <210> 256
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 256
Gly Arg Asp Ile Thr Arg Leu
 1           5

    <210> 257
    <211> 8
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 257
Gln Gly Arg Asp Ile Thr Arg Leu
 1           5

    <210> 258
    <211> 4
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 258
Ser Thr Thr Leu
 1

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    <210> 259
    <211> 5
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 259
Thr Ser Thr Thr Leu
1          5

    <210> 260
    <211> 6
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 260
His Thr Ser Thr Thr Leu
1          5

    <210> 261
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 261
Gly His Thr Ser Thr Thr Leu
1          5

    <210> 262
    <211> 8
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ motif

    <400> 262
Ser Gly His Thr Ser Thr Thr Leu
1          5

    <210> 263
    <211> 4
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> PDZ ligand

    <400> 263
Ser Ala Gly Phe
1

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<210> 264
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDZ ligand

<400> 264
 Ser Ile Val Phe
 1

<210> 265
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDZ ligand

<400> 265
 Leu Gly Ser Phe
 1

<210> 266
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDZ ligand

<400> 266
 Asp His Trp Cys
 1

<210> 267
 <211> 90
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CASK PDZ domain 1

<400> 267
 Thr Arg Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met
 1 5 10 15
 Gly Ile Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg
 20 25 30
 Ile Met His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly
 35 40 45
 Asp Glu Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val
 50 55 60
 Glu Gln Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe
 65 70 75 80
 Lys Ile Val Pro Ser Tyr Arg Thr Gln Ser
 85 90

<210> 268
 <211> 86
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MPP1 PDZ domain 1

<400> 268
 Arg Lys Val Arg Leu Ile Gln Phe Glu Lys Val Thr Glu Glu Pro Met
 1 5 10 15
 Gly Ile Thr Leu Lys Leu Asn Glu Lys Gln Ser Cys Thr Val Ala Arg
 20 25 30
 Ile Leu His Gly Gly Met Ile His Arg Gln Gly Ser Leu His Val Gly
 35 40 45
 Asp Glu Ile Leu Glu Ile Asn Gly Thr Asn Val Thr Asn His Ser Val
 50 55 60
 Asp Gln Leu Gln Lys Ala Met Lys Glu Thr Lys Gly Met Ile Ser Leu
 65 70 75 80
 Lys Val Ile Pro Asn Gln
 85

<210> 269
 <211> 95
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LIMK1 PDZ domain 1

<400> 269
 Val Thr Leu Val Ser Ile Pro Ala Ser Ser His Gly Lys Arg Gly Leu
 1 5 10 15
 Ser Val Ser Ile Asp Pro Pro His Gly Pro Pro Gly Cys Gly Thr Glu
 20 25 30
 His Ser His Thr Val Arg Val Gln Gly Val Asp Pro Gly Cys Met Ser
 35 40 45
 Pro Asp Val Lys Asn Ser Ile His Val Gly Asp Arg Ile Leu Glu Ile
 50 55 60
 Asn Gly Thr Pro Ile Arg Asn Val Pro Leu Asp Glu Ile Asp Leu Leu
 65 70 75 80
 Ile Gln Glu Thr Ser Arg Leu Leu Gln Leu Thr Leu Glu His Asp
 85 90 95

<210> 270
 <211> 91
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KIAA 0303 PDZ domain 1

<400> 270
 Pro His Gln Pro Ile Val Ile His Ser Ser Gly Lys Asn Tyr Gly Phe
 1 5 10 15
 Thr Ile Arg Ala Ile Arg Val Tyr Val Gly Asp Ser Asp Ile Tyr Thr
 20 25 30
 Val His His Ile Val Trp Asn Val Glu Glu Gly Ser Pro Ala Cys Gln
 35 40 45
 Ala Gly Leu Lys Ala Gly Asp Leu Ile Thr His Ile Asn Gly Glu Pro
 50 55 60

Val His Gly Leu Val His Thr Glu Val Ile Glu Leu Leu Leu Lys Ser
65 70 75 80
Gly Asn Lys Val Ser Ile Thr Thr Thr Pro Phe
85 90

<210> 271
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> KIAA 0807 PDZ domain 1

<400> 271
Pro Ile Ile Ile His Arg Ala Gly Lys Lys Tyr Gly Phe Thr Leu Arg
1 5 10 15
Ala Ile Arg Val Tyr Met Gly Asp Ser Asp Val Tyr Thr Val His His
20 25 30
Met Val Trp His Val Glu Asp Gly Gly Pro Ala Ser Glu Ala Gly Leu
35 40 45
Arg Gln Gly Asp Leu Ile Thr His Val Asn Gly Glu Pro Val His Gly
50 55 60
Leu Val His Thr Glu Val Val Glu Leu Ile Leu Lys Ser Gly Asn Lys
65 70 75 80
Val Ala Ile Ser Thr Thr Pro Leu Glu
85

<210> 272
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> DLG1 PDZ domain 1

<400> 272
Val Asn Gly Thr Asp Ala Asp Tyr Glu Tyr Glu Glu Ile Thr Leu Glu
1 5 10 15
Arg Gly Asn Ser Gly Leu Gly Phe Ser Ile Ala Gly Gly Thr Asp Asn
20 25 30
Pro His Ile Gly Asp Asp Ser Ser Ile Phe Ile Thr Lys Ile Ile Thr
35 40 45
Gly Gly Ala Ala Ala Gln Asp Gly Arg Leu Arg Val Asn Asp Cys Ile
50 55 60
Leu Gln Val Asn Glu Val Asp Val Arg Asp Val Thr His Ser Lys Ala
65 70 75 80
Val Glu Ala Leu Lys Glu Ala Gly Ser Ile Val Arg Leu Tyr Val Lys
85 90 95
Arg Arg Lys Pro Val Ser Glu Lys Ile Met Glu Ile Lys Leu Ile Lys
100 105 110
Gly Pro Lys Gly Leu Gly Phe Ser Ile Ala Gly Gly Val Gly Asn Gln
115 120 125
His Ile Pro Gly Asp Asn Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly
130 135 140
Gly Ala Ala His Lys Asp Gly Lys Leu Gln Ile Gly Asp Lys Leu Leu
145 150 155 160
Ala Val Asn Asn Val Cys Leu Glu Glu Val Thr His Glu Glu Ala Val
165 170 175
Thr Ala Leu Lys Asn Thr Ser Asp Phe Val Tyr Leu Lys Val Ala Lys
180 185 190

Pro Thr Ser Met Tyr Met Asn Asp Gly Tyr Ala
 195 200

<210> 273
 <211> 338
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PSD95 PDZ domains 1-3

<400> 273
 Glu Gly Glu Met Glu Tyr Glu Glu Ile Thr Leu Glu Arg Gly Asn Ser
 1 5 10 15
 Gly Leu Gly Phe Ser Ile Ala Gly Gly Thr Asp Asn Pro His Ile Gly
 20 25 30
 Asp Asp Pro Ser Ile Phe Ile Thr Lys Ile Ile Pro Gly Gly Ala Ala
 35 40 45
 Ala Gln Asp Gly Arg Leu Arg Val Asn Asp Ser Ile Leu Phe Val Asn
 50 55 60
 Glu Val Asp Val Arg Glu Val Thr His Ser Ala Val Glu Ala Leu
 65 70 75 80
 Lys Glu Ala Gly Ser Ile Val Arg Leu Tyr Val Met Arg Arg Lys Pro
 85 90 95
 Pro Ala Glu Lys Val Met Glu Ile Lys Leu Ile Lys Gly Pro Lys Gly
 100 105 110
 Leu Gly Phe Ser Ile Ala Gly Gly Val Gly Asn Gln His Ile Pro Gly
 115 120 125
 Asp Asn Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly Gly Ala Ala His
 130 135 140
 Lys Asp Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu Ala Val Asn Ser
 145 150 155 160
 Val Gly Leu Glu Asp Val Met His Glu Asp Ala Val Ala Ala Leu Lys
 165 170 175
 Asn Thr Tyr Asp Val Val Tyr Leu Lys Val Ala Lys Pro Ser Asn Ala
 180 185 190
 Tyr Leu Ser Asp Ser Tyr Ala Pro Pro Asp Ile Thr Thr Ser Tyr Ser
 195 200 205
 Gln His Leu Asp Asn Glu Ile Ser His Ser Ser Tyr Leu Gly Thr Asp
 210 215 220
 Tyr Pro Thr Ala Met Thr Pro Thr Ser Pro Arg Arg Tyr Ser Pro Val
 225 230 235 240
 Ala Lys Asp Leu Leu Gly Glu Glu Asp Ile Pro Arg Glu Pro Arg Arg
 245 250 255
 Ile Val Ile His Arg Gly Ser Thr Gly Leu Gly Phe Asn Ile Val Gly
 260 265 270
 Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe Ile Leu Ala Gly Gly
 275 280 285
 Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly Asp Gln Ile Leu Ser
 290 295 300
 Val Asn Gly Val Asp Leu Arg Asn Ala Ser His Glu Gln Ala Ala Ile
 305 310 315 320
 Ala Leu Lys Asn Ala Gly Gln Thr Val Thr Ile Ile Ala Gln Tyr Lys
 325 330 335
 Pro Glu

<210> 274
 <211> 186
 <212> PRT
 <213> Artificial Sequence

<220>

<223> NeDLG PDZ domains 1-2

<400> 274

Tyr	Glu	Glu	Ile	Val	Leu	Glu	Arg	Gly	Asn	Ser	Gly	Leu	Gly	Phe	Ser
1				5					10					15	
Ile	Ala	Gly	Gly	Ile	Asp	Asn	Pro	His	Val	Pro	Asp	Asp	Pro	Gly	Ile
			20					25					30		
Phe	Ile	Thr	Lys	Ile	Ile	Pro	Gly	Gly	Ala	Ala	Ala	Met	Asp	Gly	Arg
		35					40					45			
Leu	Gly	Val	Asn	Asp	Cys	Val	Leu	Arg	Val	Asn	Glu	Val	Glu	Val	Ser
	50					55				60					
Glu	Val	Val	His	Ser	Arg	Ala	Val	Glu	Ala	Leu	Lys	Glu	Ala	Gly	Pro
65					70					75					80
Val	Val	Arg	Leu	Val	Val	Arg	Arg	Arg	Gln	Pro	Pro	Pro	Glu	Thr	Ile
				85					90					95	
Met	Glu	Val	Asn	Leu	Leu	Lys	Gly	Pro	Lys	Gly	Leu	Gly	Phe	Ser	Ile
			100					105					110		
Ala	Gly	Gly	Ile	Gly	Asn	Gln	His	Ile	Pro	Gly	Asp	Asn	Ser	Ile	Tyr
		115					120					125			
Ile	Thr	Lys	Ile	Ile	Glu	Gly	Gly	Ala	Ala	Gln	Lys	Asp	Gly	Arg	Leu
	130					135					140				
Gln	Ile	Gly	Asp	Arg	Leu	Leu	Ala	Val	Asn	Asn	Thr	Asn	Leu	Gln	Asp
145					150					155					160
Val	Arg	His	Glu	Glu	Ala	Val	Ala	Ser	Leu	Lys	Asn	Thr	Ser	Asp	Met
				165					170					175	
Val	Tyr	Leu	Lys	Val	Ala	Lys	Pro	Gly	Ser						
			180					185							

<210> 275

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> SNTa1 PDZ domain 1

<400> 275

Gln	Arg	Arg	Arg	Val	Thr	Val	Arg	Lys	Ala	Asp	Ala	Gly	Gly	Leu	Gly
1				5					10					15	
Ile	Ser	Ile	Lys	Gly	Gly	Arg	Glu	Asn	Lys	Met	Pro	Ile	Leu	Ile	Ser
			20					25					30		
Lys	Ile	Phe	Lys	Gly	Leu	Ala	Ala	Asp	Gln	Thr	Glu	Ala	Leu	Phe	Val
		35					40					45			
Gly	Asp	Ala	Ile	Leu	Ser	Val	Asn	Gly	Glu	Asp	Leu	Ser	Ser	Ala	Thr
	50					55				60					
His	Asp	Glu	Ala	Val	Gln	Val	Leu	Lys	Lys	Thr	Gly	Lys	Glu	Val	Val
65					70					75					80
Leu	Glu	Val	Lys	Tyr	Met	Lys	Asp	Val	Ser	Pro	Tyr	Phe	Lys		
				85					90						

<210> 276

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> TAX-IP 43 PDZ domain 1

<400> 276
 Gln Lys Arg Gly Val Lys Val Leu Lys Gln Glu Leu Gly Gly Leu Gly
 1 5 10 15
 Ile Ser Ile Lys Gly Gly Lys Glu Asn Lys Met Pro Ile Leu Ile Ser
 20 25 30
 Lys Ile Phe Lys Gly Leu Ala Ala Asp Gln Thr Gln Ala Leu Tyr Val
 35 40 45
 Gly Asp Ala Ile Leu Ser Val Asn Gly Ala Asp Leu Arg Asp Ala Thr
 50 55 60
 His Asp Glu Ala Val Gln Ala Leu
 65 70

<210> 277
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LDP PDZ domain 1

<400> 277
 Arg Gly Met Thr Thr Gln Gln Ile Asp Leu Gln Gly Pro Gly Pro Trp
 1 5 10 15
 Gly Phe Arg Leu Val Gly Arg Lys Asp Phe Glu Gln Pro Leu Ala Ile
 20 25 30
 Ser Arg Val Thr Pro Gly Ser Lys Ala Ala Leu
 35 40

<210> 278
 <211> 84
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LIM PDZ domain 1

<400> 278
 Ser Asn Tyr Ser Val Ser Leu Val Gly Pro Ala Pro Trp Gly Phe Arg
 1 5 10 15
 Leu Gln Gly Gly Lys Asp Phe Asn Met Pro Leu Thr Ile Ser Ser Leu
 20 25 30
 Lys Asp Gly Gly Lys Ala Ala Gln Ala Asn Val Arg Ile Gly Asp Val
 35 40 45
 Val Leu Ser Ile Asp Gly Ile Asn Ala Gln Gly Met Thr His Leu Glu
 50 55 60
 Ala Gln Asn Lys Ile Lys Gly Cys Thr Gly Ser Leu Asn Met Thr Leu
 65 70 75 80
 Gln Arg Ala Ser

<210> 279
 <211> 178
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MINT1 PDZ domains 1-2

<400> 279
 Ser Glu Asn Cys Lys Asp Val Phe Ile Glu Lys Gln Lys Gly Glu Ile
 1 5 10 15

Leu Gly Val Val Ile Val Glu Ser Gly Trp Gly Ser Ile Leu Pro Thr
 20 25 30
 Val Ile Ile Ala Asn Met Met His Gly Gly Pro Ala Glu Lys Ser Gly
 35 40 45
 Lys Leu Asn Ile Gly Asp Gln Ile Met Ser Ile Asn Gly Thr Ser Leu
 50 55 60
 Val Gly Leu Pro Leu Ser Thr Cys Gln Ser Ile Ile Lys Gly Leu Glu
 65 70 75 80
 Asn Gln Ser Arg Val Lys Leu Asn Ile Val Arg Cys Pro Pro Val Thr
 85 90 95
 Thr Val Leu Ile Arg Arg Pro Asp Leu Arg Tyr Gln Leu Gly Phe Ser
 100 105 110
 Val Gln Asn Gly Ile Ile Cys Ser Leu Met Arg Gly Gly Ile Ala Glu
 115 120 125
 Arg Gly Gly Val Arg Val Gly His Arg Ile Ile Glu Ile Asn Gly Gln
 130 135 140
 Ser Val Val Ala Thr Pro His Glu Lys Ile Val His Ile Leu Ser Asn
 145 150 155 160
 Ala Val Gly Glu Ile His Met Lys Thr Met Pro Ala Ala Met Tyr Arg
 165 170 175
 Leu Leu

<210> 280
 <211> 187
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> X11 beta PDZ domains 1-2

<400> 280
 His Phe Ser Asn Ser Glu Asn Cys Lys Glu Leu Gln Leu Glu Lys His
 1 5 10 15
 Lys Gly Glu Ile Leu Gly Val Val Val Val Glu Ser Gly Trp Gly Ser
 20 25 30
 Ile Leu Pro Thr Val Ile Leu Ala Asn Met Met Asn Gly Cys Pro Ala
 35 40 45
 Ala Arg Ser Gly Lys Leu Ser Ile Gly Asp Gln Ile Met Ser Ile Asn
 50 55 60
 Gly Thr Ser Leu Val Gly Leu Pro Leu Ala Thr Cys Gln Gly Ile Ile
 65 70 75 80
 Lys Gly Leu Lys Asn Gln Thr Gln Val Lys Leu Asn Ile Val Ser Cys
 85 90 95
 Pro Pro Val Thr Thr Val Leu Ile Lys Arg Pro Asp Leu Lys Tyr Gln
 100 105 110
 Leu Gly Phe Ser Val Gln Asn Gly Ile Ile Cys Ser Leu Met Arg Gly
 115 120 125
 Gly Ile Ala Glu Arg Gly Gly Val Arg Val Gly His Arg Ile Ile Glu
 130 135 140
 Ile Asn Gly Gln Ser Val Val Ala Thr Ala His Glu Lys Ile Val Gln
 145 150 155 160
 Ala Leu Ser Asn Ser Val Gly Glu Ile His Met Lys Thr Met Pro Ala
 165 170 175
 Ala Met Phe Arg Leu Leu Thr Gly Gln Glu Asn
 180 185

<210> 281
 <211> 80
 <212> PRT
 <213> Artificial Sequence

<220>

<223> KIAA 0440 PDZ domain 1

<400> 281

Ser	Ser	Val	Glu	Met	Thr	Leu	Arg	Arg	Asn	Gly	Leu	Gly	Gln	Leu	Gly
1				5					10				15		
Phe	His	Val	Asn	Tyr	Glu	Gly	Ile	Val	Ala	Asp	Val	Glu	Pro	Tyr	Gly
			20					25				30			
Tyr	Ala	Trp	Gln	Ala	Gly	Leu	Arg	Gln	Gly	Ser	Arg	Leu	Val	Glu	Ile
		35				40					45				
Cys	Lys	Val	Ala	Val	Ala	Thr	Leu	Ser	His	Glu	Gln	Met	Ile	Asp	Leu
	50					55				60					
Leu	Arg	Thr	Ser	Val	Thr	Val	Lys	Val	Val	Ile	Ile	Pro	Pro	His	Glu
65					70					75					80

<210> 282

<211> 83

<212> PRT

<213> Artificial Sequence

<220>

<223> KIAA 0545 PDZ domain 1

<400> 282

Ser	Gly	Trp	Glu	Thr	Val	Asp	Met	Thr	Leu	Arg	Arg	Asn	Gly	Leu	Gly
1				5				10					15		
Gln	Leu	Gly	Phe	His	Val	Lys	Tyr	Asp	Gly	Thr	Val	Ala	Glu	Val	Glu
			20					25				30			
Asp	Tyr	Gly	Phe	Ala	Trp	Gln	Ala	Gly	Leu	Arg	Gln	Gly	Ser	Arg	Leu
		35				40					45				
Val	Glu	Ile	Cys	Lys	Val	Ala	Val	Val	Thr	Leu	Thr	His	Asp	Gln	Met
	50					55				60					
Ile	Asp	Leu	Leu	Arg	Thr	Ser	Val	Thr	Val	Lys	Val	Val	Ile	Ile	Pro
65					70					75					80
Pro	Phe	Glu													

<210> 283

<211> 86

<212> PRT

<213> Artificial Sequence

<220>

<223> TAX-IP2 PDZ domain 1

<400> 283

Arg	Lys	Glu	Val	Glu	Val	Phe	Lys	Ser	Glu	Asp	Ala	Leu	Gly	Leu	Thr
1				5				10					15		
Ile	Thr	Asp	Asn	Gly	Ala	Gly	Tyr	Ala	Phe	Ile	Lys	Arg	Ile	Lys	Glu
			20					25				30			
Gly	Ser	Val	Ile	Asp	His	Ile	His	Leu	Ile	Ser	Val	Gly	Asp	Met	Ile
		35				40					45				
Glu	Ala	Ile	Asn	Gly	Gln	Ser	Leu	Leu	Gly	Cys	Arg	His	Tyr	Glu	Val
	50					55				60					
Ala	Arg	Leu	Leu	Lys	Glu	Leu	Pro	Arg	Gly	Arg	Thr	Phe	Thr	Leu	Lys
65					70					75					80
Leu	Thr	Glu	Pro	Arg	Lys										
					85										

<210> 284
 <211> 93
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TAX-IP 2-like PDZ domain 1

<400> 284
 Ile Arg Gly Glu Thr Lys Glu Val Glu Val Thr Lys Thr Glu Asp Ala
 1 5 10 15
 Leu Gly Leu Thr Ile Thr Asp Asn Gly Ala Gly Tyr Ala Phe Ile Lys
 20 25 30
 Arg Ile Lys Glu Gly Ser Ile Ile Asn Arg Ile Glu Ala Val Cys Val
 35 40 45
 Gly Asp Ser Ile Glu Ala Ile Asn Asp His Ser Ile Val Gly Cys Arg
 50 55 60
 His Tyr Glu Val Ala Lys Met Leu Arg Glu Leu Pro Lys Ser Gln Pro
 65 70 75 80
 Phe Thr Leu Arg Leu Val Gln Pro Lys Arg Ala Phe Glu
 85 90

<210> 285
 <211> 91
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TAX-IP 33 PDZ domain 1

<400> 285
 His Ser His Pro Arg Val Val Glu Leu Pro Lys Thr Asp Glu Gly Leu
 1 5 10 15
 Gly Phe Asn Val Met Gly Gly Lys Glu Gln Asn Ser Pro Ile Tyr Ile
 20 25 30
 Ser Arg Ile Ile Pro Gly Gly Val Ala Glu Arg His Gly Gly Leu Lys
 35 40 45
 Arg Gly Asp Gln Leu Leu Ser Val Asn Gly Val Ser Val Glu Gly Glu
 50 55 60
 His His Glu Lys Ala Val Glu Leu Leu Lys Ala Ala Lys Asp Ser Val
 65 70 75 80
 Lys Leu Val Val Arg Tyr Thr Pro Lys Val Leu
 85 90

<210> 286
 <211> 89
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MPP2 PDZ domain 1

<400> 286
 Pro Val Pro Pro Asp Ala Val Arg Met Val Gly Ile Arg Lys Thr Ala
 1 5 10 15
 Gly Glu His Leu Gly Val Thr Phe Arg Val Glu Gly Gly Glu Leu Val
 20 25 30
 Ile Ala Arg Ile Leu His Gly Gly Met Val Ala Gln Gln Gly Leu Leu
 35 40 45
 His Val Gly Asp Ile Ile Lys Glu Val Asn Gly Gln Pro Val Gly Ser
 50 55 60

Asp Pro Arg Ala Leu Gln Glu Leu Leu Arg Asn Ala Ser Gly Ser Val
65 70 75 80
Ile Leu Lys Ile Leu Pro Asn Tyr Gln
85

<210> 287
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> MINT3 PDZ domain 1

<400> 287
Pro Val Thr Thr Ala Ile Ile His Arg Pro His Ala Arg Glu Gln Leu
1 5 10 15
Gly Phe Cys Val Glu Asp Gly Ile Val Arg Pro Arg Pro Leu Ala Pro
20 25 30
Gly Trp Gly Gly Arg Ala Ala Leu Ser Thr
35 40

<210> 288
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> TIP-1 PDZ domain 1

<400> 288
Gln Arg Val Glu Ile His Lys Leu Arg Gln Gly Glu Asn Leu Ile Leu
1 5 10 15
Gly Phe Ser Ile Gly Gly Gly Ile Asp Gln Asp Pro Ser Gln Asn Pro
20 25 30
Phe Ser Glu Asp Lys Thr Asp Lys Gly Ile Tyr Val Thr Arg Val Ser
35 40 45
Glu Gly Gly Pro Ala Glu Ile Ala Gly Leu Gln Ile Gly Asp Lys Ile
50 55 60
Met Gln Val Asn Gly Trp Asp Met Thr Met Val Thr His Asp Gln Ala
65 70 75 80
Arg Lys Arg Leu Thr Lys Arg Ser Glu Glu Val Val Arg Leu Leu Val
85 90 95
Thr Arg Gln Ser Leu Gln Lys
100

<210> 289
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> PTN-4 PDZ domain 1

<400> 289
Leu Ile Arg Met Lys Pro Asp Glu Asn Gly Arg Phe Gly Phe Asn Val
1 5 10 15
Lys Gly Gly Tyr Asp Gln Lys Met Pro Val Ile Val Ser Arg Val Ala
20 25 30
Pro Gly Thr Pro Ala Asp Leu Cys Val Pro Arg Leu Asn Glu Gly Asp
35 40 45

Gln Val Val Leu Ile Asn Gly Arg Asp Ile Ala Glu His Thr His Asp
50 55 60
Gln Val Val Leu Phe Ile Lys Ala Ser Cys Glu Arg His Ser Gly Glu
65 70 75 80
Leu Met Leu Leu Val Arg Pro Asn Ala
85

<210> 290
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> prIL16 PDZ domain 1

<400> 290
Ile His Val Thr Ile Leu His Lys Glu Glu Gly Ala Gly Leu Gly Phe
1 5 10 15
Ser Leu Ala Gly Gly Ala Asp Leu Glu Asn Lys Val Ile Thr Val His
20 25 30
Arg Val Phe Pro Asn Gly Leu Ala Ser Gln Glu Gly Thr Ile Gln Lys
35 40 45
Gly Asn Glu Val Leu Ser Ile Asn Gly Lys Ser Leu Lys Gly Thr Thr
50 55 60
His His Asp Ala Leu Ala Ile Leu Arg Gln Ala Arg Glu Pro Arg Gln
65 70 75 80
Ala Val Ile Val Thr Arg Lys Leu Thr Pro Glu Ala Met Pro Asp Leu
85 90 95
Asn Ser Ser Thr Asp Ser Ala Ala Ser Ala Ser Ala Ala Ser Asp Val
100 105 110
Ser Val Glu Ser Thr Ala Glu Ala Thr Val Cys Thr Val Thr Leu Glu
115 120 125
Lys Met Ser Ala Gly Leu Gly Phe Ser Leu Glu Gly Gly Lys Gly Ser
130 135 140
Leu His Gly Asp Lys Pro Leu Thr Ile Asn Arg Ile Phe Lys Gly Ala
145 150 155 160
Ala Ser Glu Gln Ser Glu Thr Val Gln Pro Gly Asp Glu Ile Leu Gln
165 170 175
Leu Gly Gly Thr Ala Met Gln Gly Leu Thr Arg Phe Glu Ala Trp Asn
180 185 190
Ile Ile Lys Ala Leu Pro Asp Gly Pro Val Thr Ile Val Ile Arg Arg
195 200 205
Lys Ser Leu Gln Ser Lys
210

<210> 291
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> CBP PDZ domain 1

<400> 291
Gln Arg Lys Leu Val Thr Val Glu Lys Gln Asp Asn Glu Thr Phe Gly
1 5 10 15
Phe Glu Ile Gln Ser Tyr Arg Pro Gln Asn Gln Asn Ala Cys Ser Ser
20 25 30
Glu Met Phe Thr Leu Ile Cys Lys Ile Gln Glu Asp Ser Pro Ala His
35 40 45

Cys Ala Gly Leu Gln Ala Gly Asp Val Leu Ala Asn Ile Asn Gly Val
50 55 60
Ser Thr Glu Gly Phe Thr Tyr Lys Gln Val Val Asp Leu Ile Arg Ser
65 70 75 80
Ser Gly Asn Leu Leu Thr Ile Glu Thr Leu Asn Gly
85 90

<210> 292
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> KIAA 0751 PDZ domain 1

<400> 292
Arg Asp Ser Gly Ala Met Leu Gly Leu Lys Val Val Gly Gly Lys Met
1 5 10 15
Thr Glu Ser Gly Arg Leu Cys Ala Phe Ile Thr Lys Val Lys Lys Gly
20 25 30
Ser Leu Ala Asp Thr Val Gly His Leu Arg Pro Gly Asp Glu Val Leu
35 40 45
Glu Trp Asn Gly Arg Leu Leu Gln Gly Ala Thr Phe Glu Glu Val Tyr
50 55 60
Asn Ile Ile Leu Glu Ser Lys Pro Glu Pro Gln Val Glu Leu Val Val
65 70 75 80
Ser Arg

<210> 293
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> KIAA 0559 PDZ domain 1

<400> 293
His Tyr Ile Phe Pro His Ala Arg Ile Lys Ile Thr Arg Asp Ser Lys
1 5 10 15
Asp His Thr Val Ser Gly Asn Gly Leu Gly Ile Arg Ile Val Gly Gly
20 25 30
Lys Glu Ile Pro Gly His Ser Gly Glu Ile Gly Ala Tyr Ile Ala Lys
35 40 45
Ile Leu Pro Gly Gly Ser Ala Glu Gln Thr Gly Lys Leu Met Glu Gly
50 55 60
Met Gln Val Leu Glu Trp Asn Gly Ile Pro Leu Thr Ser Lys Thr Tyr
65 70 75 80
Glu Glu Val Gln Ser Ile Ile Ser Gln Gln Ser Gly Glu Ala Glu Ile
85 90 95
Cys Val Arg Leu Asp Leu Asn Met Leu
100 105

<210> 294
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> AF6 PDZ domain 1

<400> 294
 Leu Arg Lys Glu Pro Glu Ile Ile Thr Val Thr Leu Lys Lys Gln Asn
 1 5 10 15
 Gly Met Gly Leu Ser Ile Val Ala Ala Lys Gly Ala Gly Gln Asp Lys
 20 25 30
 Leu Gly Ile Tyr Val Lys Ser Val Val Lys Gly Gly Ala Ala Asp Val
 35 40 45
 Asp Gly Arg Leu Ala Ala Gly Asp Gln Leu Leu Ser Val Asp Gly Arg
 50 55 60
 Ser Leu Val Gly Leu Ser Gln Glu Arg Ala Ala Glu Leu Met Thr Arg
 65 70 75 80
 Thr Ser Ser Val Val Thr Leu Glu Val Ala Lys Gln Gly
 85 90

<210> 295
 <211> 90
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PICK1 PDZ domain 1

<400> 295
 Pro Thr Val Pro Gly Lys Val Thr Leu Gln Lys Asp Ala Gln Asn Leu
 1 5 10 15
 Ile Gly Ile Ser Ile Gly Gly Gly Ala Gln Tyr Cys Pro Cys Leu Tyr
 20 25 30
 Ile Val Gln Val Phe Asp Asn Thr Pro Ala Ala Leu Asp Gly Thr Val
 35 40 45
 Ala Ala Gly Asp Glu Ile Thr Gly Val Asn Gly Arg Ser Ile Lys Gly
 50 55 60
 Lys Thr Lys Val Glu Val Ala Lys Met Ile Gln Glu Val Lys Gly Glu
 65 70 75 80
 Val Thr Ile His Tyr Asn Lys Leu Gln Glu
 85 90

<210> 296
 <211> 69
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> RGS12 PDZ domain 1

<400> 296
 Pro Pro Arg Val Arg Ser Val Glu Val Ala Arg Gly Arg Ala Gly Tyr
 1 5 10 15
 Gly Phe Thr Leu Ser Gly Gln Ala Pro Cys Val Leu Ser Cys Val Met
 20 25 30
 Arg Gly Ser Pro Ala Asp Phe Val Gly Leu Arg Ala Gly Asp Gln Ile
 35 40 45
 Leu Ala Val Asn Glu Ile Asn Val Lys Lys Ala Ser His Glu Asp Val
 50 55 60
 Val Lys Leu Ile Gly
 65

<210> 297
 <211> 324
 <212> PRT
 <213> Artificial Sequence

<220>

<223> PDZK1 PDZ domain 2-4

<400> 297

```
Arg Leu Cys Tyr Leu Val Lys Glu Gly Gly Ser Tyr Gly Phe Ser Leu
 1          5          10          15
Lys Thr Val Gln Gly Lys Lys Gly Val Tyr Met Thr Asp Ile Thr Pro
 20          25          30
Gln Gly Val Ala Met Arg Ala Gly Val Leu Ala Asp Asp His Leu Ile
 35          40          45
Glu Val Asn Gly Glu Asn Val Glu Asp Ala Ser His Glu Lys Val Val
 50          55          60
Glu Lys Val Lys Lys Ser Gly Ser Arg Val Met Phe Leu Leu Val Asp
 65          70          75          80
Lys Glu Thr Asp Lys Arg His Val Glu Gln Lys Ile Gln Phe Lys Arg
 85          90          95
Glu Thr Ala Ser Leu Lys Leu Leu Pro His Gln Pro Arg Ile Val Glu
100          105          110
Met Lys Lys Gly Ser Asn Gly Tyr Gly Phe Tyr Leu Arg Ala Gly Ser
115          120          125
Glu Gln Lys Gly Gln Ile Ile Lys Asp Ile Asp Ser Gly Ser Pro Ala
130          135          140
Glu Glu Ala Gly Leu Lys Asn Asn Asp Leu Val Val Ala Val Asn Gly
145          150          155          160
Glu Ser Val Glu Thr Leu Asp His Asp Ser Val Val Glu Met Ile Arg
165          170          175
Lys Gly Gly Asp Gln Thr Ser Leu Leu Val Val Asp Lys Glu Thr Asp
180          185          190
Asn Met Tyr Arg Leu Ala His Phe Ser Pro Phe Leu Tyr Tyr Gln Ser
195          200          205
Gln Glu Leu Pro Asn Gly Ser Val Lys Glu Ala Pro Ala Pro Thr Pro
210          215          220
Thr Ser Leu Glu Val Ser Ser Pro Pro Asp Thr Thr Glu Glu Val Asp
225          230          235          240
His Lys Pro Lys Leu Cys Arg Leu Ala Lys Gly Glu Asn Gly Tyr Gly
245          250          255
Phe His Leu Asn Ala Ile Arg Gly Leu Pro Gly Ser Phe Ile Lys Glu
260          265          270
Val Gln Lys Gly Gly Pro Ala Asp Leu Ala Gly Leu Glu Asp Glu Asp
275          280          285
Val Ile Ile Glu Val Asn Gly Val Asn Val Leu Asp Glu Pro Tyr Glu
290          295          300
Lys Val Val Asp Arg Ile Gln Ser Ser Gly Lys Asn Val Thr Leu Leu
305          310          315          320
Val Cys Gly Lys
```

<210> 298

<211> 88

<212> PRT

<213> Artificial Sequence

<220>

<223> KIAA 0316 PDZ domain 1

<400> 298

```
Ile Pro Pro Ala Pro Arg Lys Val Glu Met Arg Arg Asp Pro Val Leu
 1          5          10          15
Gly Phe Gly Phe Val Ala Gly Ser Glu Lys Pro Val Val Val Arg Ser
 20          25          30
```

Val	Thr	Pro	Gly	Gly	Pro	Ser	Glu	Gly	Lys	Leu	Ile	Pro	Gly	Asp	Gln
		35					40					45			
Ile	Val	Met	Ile	Asn	Asp	Glu	Pro	Val	Ser	Ala	Ala	Pro	Arg	Glu	Arg
	50					55					60				
Val	Ile	Asp	Leu	Val	Arg	Ser	Cys	Lys	Glu	Ser	Ile	Leu	Leu	Thr	Val
65					70					75					80
Ile	Gln	Pro	Tyr	Pro	Ser	Pro	Lys								
				85											

<210> 299
 <211> 241
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DLG5 PDZ domain 2

Pro	Tyr	Val	Glu	Glu	Pro	Arg	His	Val	Lys	Val	Gln	Lys	Gly	Ser	Glu
1			5						10					15	
Pro	Leu	Gly	Ile	Ser	Ile	Val	Ser	Gly	Glu	Lys	Gly	Gly	Ile	Tyr	Val
			20					25					30		
Ser	Lys	Val	Thr	Val	Gly	Ser	Ile	Ala	His	Gln	Ala	Gly	Leu	Glu	Tyr
		35				40					45				
Gly	Asp	Gln	Leu	Leu	Glu	Phe	Asn	Gly	Ile	Asn	Leu	Arg	Ser	Ala	Thr
	50					55				60					
Glu	Gln	Gln	Ala	Arg	Leu	Ile	Ile	Gly	Gln	Gln	Cys	Asp	Thr	Ile	Thr
65					70				75						80
Ile	Leu	Ala	Gln	Tyr	Asn	Pro	His	Val	His	Gln	Leu	Ser	Ser	His	Ser
			85					90						95	
Arg	Ser	Ser	Ser	His	Leu	Asp	Pro	Ala	Gly	Thr	His	Ser	Thr	Leu	Gln
			100					105					110		
Gly	Ser	Gly	Thr	Thr	Thr	Pro	Glu	His	Pro	Ser	Val	Ile	Asp	Pro	Leu
		115					120					125			
Met	Glu	Gln	Asp	Glu	Gly	Pro	Ser	Thr	Pro	Pro	Ala	Lys	Gln	Ser	Ser
	130					135					140				
Ser	Arg	Ile	Ala	Gly	Asp	Ala	Asn	Lys	Lys	Thr	Leu	Glu	Pro	Arg	Val
145					150					155					160
Val	Phe	Ile	Lys	Lys	Ser	Gln	Leu	Glu	Leu	Gly	Val	His	Leu	Cys	Gly
			165					170						175	
Gly	Asn	Leu	His	Gly	Val	Phe	Val	Ala	Glu	Val	Glu	Asp	Asp	Ser	Pro
			180					185					190		
Ala	Lys	Gly	Pro	Asp	Gly	Leu	Val	Pro	Gly	Asp	Leu	Ile	Leu	Glu	Tyr
		195					200					205			
Gly	Ser	Leu	Asp	Val	Arg	Asn	Lys	Thr	Val	Glu	Glu	Val	Tyr	Val	Glu
	210					215					220				
Met	Leu	Lys	Pro	Arg	Asp	Gly	Val	Arg	Leu	Lys	Val	Gln	Tyr	Arg	Pro
225					230					235					240
Glu															

<210> 300
 <211> 181
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SYNT aa 67-241

<400> 300

Arg	Glu	Ile	Lys	Gln	Gly	Ile	Arg	Glu	Val	Ile	Leu	Cys	Lys	Asp	Gln
1				5				10						15	
Asp	Gly	Lys	Ile	Gly	Leu	Arg	Leu	Lys	Ser	Ile	Asp	Asn	Gly	Ile	Phe
			20					25					30		
Val	Gln	Leu	Val	Gln	Ala	Asn	Ser	Pro	Ala	Ser	Leu	Val	Gly	Leu	Arg
		35					40					45			
Phe	Gly	Asp	Gln	Val	Leu	Gln	Ile	Asn	Gly	Glu	Asn	Cys	Ala	Gly	Trp
		50				55					60				
Ser	Ser	Asp	Lys	Ala	His	Lys	Val	Leu	Lys	Gln	Ala	Phe	Gly	Glu	Lys
65					70					75					80
Ile	Thr	Met	Thr	Ile	Arg	Asp	Arg	Pro	Phe	Glu	Arg	Thr	Val	Ile	Met
				85					90					95	
His	Lys	Asp	Ser	Ser	Gly	His	Val	Gly	Phe	Ile	Phe	Lys	Ser	Gly	Lys
			100					105					110		
Ile	Thr	Ser	Ile	Val	Lys	Asp	Ser	Ser	Ala	Ala	Arg	Asn	Gly	Leu	Leu
		115					120					125			
Thr	Asp	His	His	Ile	Cys	Glu	Ile	Asn	Gly	Gln	Asn	Val	Ile	Gly	Leu
	130					135					140				
Lys	Asp	Ala	Gln	Ile	Ala	Asp	Ile	Leu	Ser	Thr	Ala	Gly	Thr	Val	Val
145					150					155					160
Thr	Ile	Thr	Ile	Met	Pro	Thr	Phe	Ile	Phe	Glu	His	Ile	Ile	Lys	Arg
				165					170					175	
Met	Ala	Pro	Ser	Met											
			180												

<210> 301

<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> WWP3 (MAGI-1) PDZ domains 1-2

<400> 301

Pro	Ser	Glu	Leu	Lys	Gly	Lys	Phe	Ile	His	Thr	Lys	Leu	Arg	Lys	Ser
1				5				10						15	
Ser	Arg	Gly	Phe	Gly	Phe	Thr	Val	Val	Gly	Gly	Asp	Glu	Pro	Asp	Glu
			20					25					30		
Phe	Leu	Gln	Ile	Lys	Ser	Leu	Val	Leu	Asp	Gly	Pro	Ala	Ala	Leu	Asp
		35					40					45			
Gly	Lys	Met	Glu	Thr	Gly	Asp	Val	Ile	Val	Ser	Val	Asn	Asp	Thr	Cys
		50				55					60				
Val	Leu	Gly	His	Thr	His	Ala	Gln	Val	Val	Lys	Ile	Phe	Gln	Ser	Ile
65					70					75					80
Pro	Ile	Gly	Ala	Ser	Val	Asp	Leu	Glu	Leu	Cys	Arg	Gly	Tyr	Pro	Leu
				85				90						95	
Pro	Phe	Asp	Pro	Asp	Asp	Pro	Asn	Thr	Ser	Leu	Val	Thr	Ser	Val	Ala
			100				105						110		
Ile	Leu	Asp	Lys	Glu	Pro	Ile	Ile	Val	Asn	Gly	Gln	Glu	Thr	Tyr	Asp
		115					120					125			
Ser	Pro	Ala	Ser	His	Ser	Ser	Lys	Thr	Gly	Lys	Val	Asn	Gly	Met	Lys
		130				135					140				
Asp	Ala	Arg	Pro	Ser	Ser	Pro	Ala	Asp	Val	Ala	Ser	Asn	Ser	Ser	His
145					150					155					160
Gly	Tyr	Pro	Asn	Asp	Thr	Val	Ser	Leu	Ala	Ser	Ser	Ile	Ala	Thr	Gln
				165					170					175	
Pro	Glu	Leu	Ile	Thr	Val	His	Ile	Val	Lys	Gly	Pro	Met	Gly	Phe	Gly
			180					185					190		
Phe	Thr	Ile	Ala	Asp	Ser	Pro	Gly	Gly	Gly	Gly	Gln	Arg	Val	Lys	Gln
		195					200					205			

Ile Val Asp Ser Pro Arg Cys Arg Gly Leu Lys Glu Gly Asp Leu Ile
 210 215 220
 Val Glu Val Asn Lys Lys Asn Val Gln Ala Leu Thr His Asn Gln Val
 225 230 235 240
 Val Asp Met Leu Val Glu Cys Pro Lys Gly Ser Glu Val Thr Leu Leu
 245 250 255
 Val Gln Arg Gly Gly Leu Pro
 260

<210> 302
 <211> 103
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TAX-IP 40 PDZ domain 1

<400> 302
 Leu Leu Pro Glu Thr His Arg Arg Val Arg Leu His Lys His Gly Ser
 1 5 10 15
 Asp Arg Pro Leu Gly Phe Tyr Ile Arg Asp Gly Met Ser Val Arg Val
 20 25 30
 Ala Pro Gln Gly Leu Glu Arg Val Pro Gly Ile Phe Ile Ser Arg Leu
 35 40 45
 Val Arg Gly Gly Leu Ala Glu Ser Thr Gly Leu Leu Ala Val Ser Asp
 50 55 60
 Glu Ile Leu Glu Val Asn Gly Ile Glu Val Ala Gly Lys Thr Leu Asp
 65 70 75 80
 Gln Val Thr Asp Met Met Val Ala Asn Ser His Asn Leu Ile Val Thr
 85 90 95
 Val Lys Pro Ala Asn Gln Arg
 100

<210> 303
 <211> 94
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KIAA 0858 PDZ domain 1

<400> 303
 Phe Ser Asp Met Arg Ile Ser Ile Asn Gln Thr Pro Gly Lys Ser Leu
 1 5 10 15
 Asp Phe Gly Phe Thr Ile Lys Trp Asp Ile Pro Gly Ile Phe Val Ala
 20 25 30
 Ser Val Glu Ala Gly Ser Pro Ala Glu Phe Ser Gln Leu Gln Val Asp
 35 40 45
 Asp Glu Ile Ile Ala Ile Asn Asn Thr Lys Phe Ser Tyr Asn Asp Ser
 50 55 60
 Lys Glu Trp Glu Glu Ala Met Ala Lys Ala Gln Glu Thr Gly His Leu
 65 70 75 80
 Val Met Asp Val Arg Arg Tyr Gly Lys Ala Gly Ser Pro Glu
 85 90

<210> 304
 <211> 88
 <212> PRT
 <213> Artificial Sequence

<220>

<223> TIAM1 PDZ domain 1

<400> 304

His	Ser	Ile	His	Ile	Glu	Lys	Ser	Asp	Thr	Ala	Ala	Asp	Thr	Tyr	Gly
1				5					10					15	
Phe	Ser	Leu	Ser	Ser	Val	Glu	Glu	Asp	Gly	Ile	Arg	Arg	Leu	Tyr	Val
			20					25					30		
Asn	Ser	Val	Lys	Glu	Thr	Gly	Leu	Ala	Ser	Lys	Lys	Gly	Leu	Lys	Ala
			35				40					45			
Gly	Asp	Glu	Ile	Leu	Glu	Ile	Asn	Asn	Arg	Ala	Ala	Asp	Ala	Leu	Asn
	50					55					60				
Ser	Ser	Met	Leu	Lys	Asp	Phe	Leu	Ser	Gln	Pro	Ser	Leu	Gly	Leu	Leu
65					70				75					80	
Val	Arg	Thr	Tyr	Pro	Glu	Leu	Glu								
					85										

<210> 305

<211> 88

<212> PRT

<213> Artificial Sequence

<220>

<223> ConEn PDZ domain 1

<400> 305

Leu	Glu	Gln	Lys	Ala	Val	Leu	Glu	Gln	Val	Gln	Leu	Asp	Ser	Pro	Leu
1				5					10					15	
Gly	Leu	Glu	Ile	His	Thr	Thr	Ser	Asn	Cys	Gln	His	Phe	Val	Ser	Gln
			20					25					30		
Val	Asp	Thr	Gln	Val	Pro	Thr	Asp	Ser	Arg	Leu	Gln	Ile	Gln	Pro	Gly
		35					40					45			
Asp	Glu	Val	Val	Gln	Ile	Asn	Glu	Gln	Val	Val	Val	Gly	Trp	Pro	Arg
	50					55					60				
Lys	Asn	Met	Val	Arg	Glu	Leu	Leu	Arg	Glu	Pro	Ala	Gly	Leu	Ser	Leu
65					70				75					80	
Val	Leu	Lys	Lys	Ile	Pro	Ile	Pro								
					85										

<210> 306

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> SPSht PDZ domain 1

<400> 306

Ser	Ser	Ser	Gly	Ile	Ser	Gly	Ser	Gln	Arg	Arg	Tyr	Ile	Gly	Val	Met
1				5					10					15	
Met	Leu	Thr	Leu	Ser	Pro	Ser	Ala	Gly	Leu	Arg	Pro	Gly	Asp	Val	Ile
			20					25					30		
Leu	Ala	Ile	Gly	Glu	Gln	Met	Val	Gln	Asn	Ala	Glu	Asp	Val	Tyr	Glu
		35					40					45			
Ala	Val	Arg	Thr	Gln	Ser	Glu									
	50					55									

<210> 307

<211> 93

<212> PRT

<213> Artificial Sequence

<220>

<223> DVL1 PDZ domain 1

<400> 307

Leu	Asn	Ile	Val	Thr	Val	Thr	Leu	Asn	Met	Glu	Arg	His	His	Phe	Leu
1				5					10					15	
Gly	Ile	Ser	Ile	Val	Gly	Gln	Ser	Asn	Asp	Arg	Gly	Asp	Gly	Gly	Ile
			20					25					30		
Tyr	Ile	Gly	Ser	Ile	Met	Lys	Gly	Gly	Ala	Val	Ala	Ala	Asp	Gly	Arg
		35				40						45			
Ile	Glu	Pro	Gly	Asp	Met	Leu	Gln	Val	Asn	Asp	Val	Asn	Phe	Glu	
	50					55				60					
Asn	Met	Ser	Asn	Asp	Asp	Ala	Val	Arg	Val	Leu	Arg	Glu	Ile	Val	Ser
65					70					75					80
Gln	Thr	Gly	Pro	Ile	Ser	Leu	Thr	Val	Ala	Lys	Cys	Trp			
				85					90						

<210> 308

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> NSP (PRSS11) PDZ domain 1

<400> 308

Ile	Arg	Gln	Ala	Lys	Gly	Lys	Ala	Ile	Thr	Lys	Lys	Lys	Tyr	Ile	Gly
1				5					10					15	
Ile	Arg	Met	Met	Ser	Leu	Thr	Ser	Ser	Lys	Ala	Lys	Glu	Leu	Lys	Asp
			20					25					30		
Arg	His	Arg	Asp	Phe	Pro	Asp	Val	Ile	Ser	Gly	Ala	Tyr	Ile	Ile	Glu
		35				40						45			
Val	Ile	Pro	Asp	Thr	Pro	Ala	Glu	Ala	Gly	Gly	Leu	Lys	Glu	Asn	Asp
	50					55					60				
Val	Ile	Ile	Ser	Ile	Asn	Gly	Gln	Ser	Val	Val	Ser	Ala	Asn	Asp	Val
65					70					75					80
Ser	Asp	Val	Ile	Lys	Arg	Glu	Ser	Thr	Leu	Asn	Met	Val	Val	Arg	Arg
				85					90					95	

Gly Asn

<210> 309

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> GEF PDZ domain 1

<400> 309

Cys	Ser	Val	Met	Ile	Phe	Glu	Val	Val	Glu	Gln	Ala	Gly	Ala	Ile	Ile
1				5					10					15	
Leu	Glu	Asp	Gly	Gln	Glu	Leu	Asp	Ser	Trp	Tyr	Val	Ile	Leu	Asn	Gly
			20					25					30		
Thr	Val	Glu	Ile	Ser	His	Pro	Asp	Gly	Lys	Val	Glu	Asn	Leu	Phe	Met
		35				40						45			
Gly	Asn	Ser	Phe	Gly	Ile	Thr	Pro	Thr	Leu	Asp	Lys	Gln	Tyr	Met	His
	50					55					60				
Gly	Ile	Val	Arg	Thr	Lys	Val	Asp	Asp	Cys	Gln	Phe	Val	Cys	Ile	Ala
65					70					75					80

Gln Gln Asp Tyr Trp Arg Ile Leu Asn His Val Glu Lys Asn Thr His
85 90 95
Lys Val Glu Glu Glu Gly Glu Ile Val Met Val His
100 105

<210> 310
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> KIAA 0902 PDZ domain 1

<400> 310
Ile Leu Asn Glu Met Ile Ala Pro Val Met Arg Val Asn Tyr Gly Gln
1 5 10 15
Ser Thr Asp Ile Asn Ala Phe Val Gly Ala Val Ser Leu Ser Cys Ser
20 25 30
Asp Ser Gly Leu Trp Ala Val Glu Gly Gly Asn Lys Leu Val Cys Ser
35 40 45
Gly Leu Leu Gln Ala Ser Lys Ser Asn Leu Ile Ser Gly Ser Val Met
50 55 60
Tyr Ile Glu Glu Lys Thr Lys Thr Lys Tyr Thr Gly Asn Pro Thr Lys
65 70 75 80
Met Tyr Glu Val Val Tyr Gln Ile Gly
85

<210> 311
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> KIAA 0561 PDZ domain 1

<400> 311
Pro Pro Ser Leu Ser Thr Ala Leu Ala Arg Ser Thr Ala Ser Ala Cys
1 5 10 15
Gly Arg Ser Ala Ser Thr Trp Val Ile Ala Thr Ser Thr Leu Cys Thr
20 25 30
Thr Ser Ser Gly Val Trp Arg Thr Glu Ala Pro Pro Arg Arg Arg Ala
35 40 45
Cys Gly Leu Gly Thr Ser Ser Pro Thr Ser Thr Gly Ser Gln Cys Trp
50 55 60
Gly Trp Cys Thr Trp Thr Ser Trp Ser Cys Cys Glx Arg Ala Ala Thr
65 70 75 80
Arg Tyr Pro Cys Gly Pro Gln Pro Trp Arg
85 90

<210> 312
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> NOS1 PDZ domain 1

<400> 312
Ile Gln Pro Asn Val Ile Ser Val Arg Leu Phe Lys Arg Lys Val Gly
1 5 10 15

Gly Leu Gly Phe Leu Val Lys Glu Arg Val Ser Lys Pro Pro Val Ile
 20 25 30
 Ile Ser Asp Leu Ile Arg Gly Gly Ala Ala Glu Gln Ser Gly Leu Ile
 35 40 45
 Gln Ala Gly Asp Ile Ile Leu Ala Val Asn Gly Arg Pro Leu Val Asp
 50 55 60
 Leu Ser Tyr Asp Ser Ala Leu Glu Val Leu Arg Gly Ile Ala Ser Glu
 65 70 75 80
 Thr His Val Val Leu Ile Leu Arg Gly Pro
 85 90

<210> 313
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> forward primer 6CAF

<400> 313
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1          5          10          15
Ala Glu Val

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 Tyr Ala Glu Val
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 Ser Pro Ile

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 Thr Ser Glu Ile
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 1 5 10 15
 Lys Ile Gly Val
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<210> 418
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 Lys Lys Gly Thr Tyr Leu Thr Asp Glu Thr His Arg Glu Val Lys Phe
 1 5 10 15
 Thr Ser Leu

<210> 419
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<210> 420
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 1 5 10 15
 Ser Asp Ala

<210> 421
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<220>
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<400> 421
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 1 5 10 15
 Gln Ser Leu Val
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<210> 422
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<220>
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<210> 423
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 Tyr Ala Ala

<210> 424
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<210> 425
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<210> 432
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 <223> PL peptide

<400> 433
 Ile Ser Lys Leu Gly Ile Ser Gly Asp Ile Asp Leu Thr Ser Ala Ser
 1 5 10 15
 Tyr Thr Met Ile
 20

<210> 434
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 434
 Leu Asn Phe Pro Leu Leu Gln Gly Ile Arg Val His Gly Met Glu Ala
 1 5 10 15
 Leu Gly Ser Phe
 20

<210> 435
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 435
 Glu Val Ile Cys Tyr Ile Glu Lys Pro Gly Val Glu Thr Leu Glu Asp
 1 5 10 15
 Ser Val Phe

<210> 436
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> PL peptide

<400> 436
Ala Arg His Arg Val Thr Ser Tyr Thr Ser Ser Ser Val Asn Val Ser
1 5 10 15
Ser Asn Leu

<210> 437
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> PL peptide

<400> 437
Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser
1 5 10 15
Thr Thr Leu

<210> 438
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> PL peptide

<400> 438
Ala Trp Asp Asp Ser Ala Arg Ala Ala Gly Gly Gln Gly Leu His Val
1 5 10 15
Thr Ala Leu

<210> 439
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> PL peptide

<400> 439
Gly Thr Ser Asp Met Lys Asp Leu Val Gly Asn Ile Glu Gln Asn Glu
1 5 10 15
His Ser Val Ile
20

<210> 440
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> PL peptide

<400> 440
Ser Phe Pro Pro Cys Gly His Arg Glu Asn Val Pro Gly Gln Ser Leu
1 5 10 15
Val Ser Phe Val
20

<210> 441
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> PL peptide

<400> 441
Thr Thr Asn Asn Asn Pro Asn Ser Ala Val Asn Ile Lys Lys Ile Phe
1 5 10 15
Thr Asp Val

<210> 442
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> PL peptide

<400> 442
Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Lys Met Pro Ser Ile
1 5 10 15
Glu Ser Asp Val
20

<210> 443
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> PL peptide

<400> 443
Thr Phe Ala Ala Gly Phe Asn Ser Thr Gly Leu Pro His Ser Thr Thr
1 5 10 15
Arg Val

<210> 444
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> PL peptide

<400> 444
 Gln Gly Asp Pro Ala Leu Gln Asp Ala Gly Asp Ser Ser Arg Lys Glu
 1 5 10 15
 Tyr Phe Ile

<210> 445
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 445
 Ser Ser Ala Lys Ser Ser Asn Lys Asn Lys Lys Asn Lys Asp Lys Glu
 1 5 10 15
 Tyr Tyr Val

<210> 446
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 446
 Gly Glu Arg Lys Pro Ser Ser Ala Ala Tyr Gln Lys Ala Pro Thr Lys
 1 5 10 15
 Glu Phe Tyr Ala
 20

<210> 447
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 447
 Leu Ala Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp Ser Leu
 1 5 10 15
 Ser Thr Asp Leu
 20

<210> 448
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 448
 Leu Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu
 1 5 10 15
 Ser Ala Gly Phe
 20

<210> 449
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> PL peptide

 <400> 449
 Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp
 1 5 10 15
 Lys Glu Gly Ala
 20

 <210> 450
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> PL peptide

 <400> 450
 Leu Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu
 1 5 10 15
 Ser Ile Val Phe
 20

 <210> 451
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> PL peptide

 <400> 451
 Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr Met Asp His Asp Leu
 1 5 10 15
 His Asp Ala Leu
 20

 <210> 452
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> PL peptide

 <400> 452
 Pro Ser Trp Arg Arg Ser Ser Leu Ser Glu Ser Glu Asn Ala Thr Ser
 1 5 10 15
 Leu Thr Thr Phe
 20

 <210> 453
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

 <400> 453
 Ser Ser Gly Gly Arg Ala Arg His Ser Tyr His His Pro Asp Gln Asp
 1 5 10 15
 His Trp Cys

<210> 454
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

 <400> 454
 Val Thr Ser Pro Asn Lys His Leu Gly Leu Val Thr Pro His Lys Thr
 1 5 10 15
 Glu Leu Val

<210> 455
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

 <400> 455
 Ser Ser Ser Gln Ser Leu Glu Ser Asp Gly Ser Tyr Gln Lys Pro Ser
 1 5 10 15
 Tyr Ile Leu

<210> 456
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

 <400> 456
 Ser Met Gln Pro Asp Asn Ser Ser Asp Ser Asp Tyr Asp Leu His Gly
 1 5 10 15
 Ala Gln Arg Leu
 20

<210> 457
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 457
 Thr Ile Tyr Glu Asn Leu Ala Pro Val Thr Thr Phe Gly Lys Thr Ile
 1 5 10 15
 Ala

<210> 458
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 458
 Gln Ile Ser Pro Gly Gly Leu Glu Pro Pro Ser Glu Lys His Phe Arg
 1 5 10 15
 Glu Thr Glu Val
 20

<210> 459
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 459
 Ser Trp Arg Arg Ser Ser Leu Ser Glu Ser Glu Asn Ala Thr Ser Leu
 1 5 10 15
 Thr Thr Phe

<210> 460
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PL peptide

<400> 460
 Lys Glu Asn Asp Tyr Glu Ser Ile Ser Asp Leu Gln Gln Gly Arg Asp
 1 5 10 15
 Ile Thr Arg Leu
 20

<210> 461
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PDZ ligand

<400> 461
 Lys Glu Gly Ala
 1

<210> 462
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> linker

<400> 462
 Leu Gln Ser Thr Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr
 1 5 10 15

<210> 463
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> linker

<400> 463
 Leu Asp Pro Gly Tyr Pro Pro Val Ala Thr
 1 5 10

<210> 464
 <211> 341
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DVL1 Construct (N-P)

<400> 464
 Met Ala Glu Thr Lys Ile Ile Tyr His Met Asp Glu Glu Glu Thr Pro
 1 5 10 15
 Tyr Leu Val Lys Leu Pro Val Ala Pro Glu Arg Val Thr Leu Ala Asp
 20 25 30
 Phe Lys Asn Val Leu Ser Asn Arg Pro Val His Ala Tyr Lys Phe Phe
 35 40 45
 Lys Ser Met Asp Gln Asp Phe Gly Val Val Lys Glu Glu Ile Phe Asp
 50 55 60
 Asp Asn Ala Lys Leu Pro Cys Phe Asn Gly Arg Val Val Ser Trp Leu
 65 70 75 80
 Val Leu Val Glu Gly Ala His Ser Asp Ala Gly Ser Gln Gly Thr Asp
 85 90 95
 Ser His Thr Asp Leu Pro Pro Pro Leu Glu Arg Thr Gly Gly Ile Gly
 100 105 110
 Asp Ser Arg Ser Pro Ser Phe Gln Pro Asp Val Ala Ser Ser Arg Asp
 115 120 125
 Gly Met Asp Asn Glu Thr Gly Thr Glu Ser Met Val Ser His Arg Arg
 130 135 140
 Asp Arg Ala Arg Arg Arg Asn Arg Glu Glu Ala Ala Arg Thr Asn Gly
 145 150 155 160
 His Pro Arg Gly Asp Arg Arg Arg Asp Val Gly Leu Pro Pro Asp Ser
 165 170 175
 Ala Ser Thr Ala Leu Ser Ser Glu Leu Glu Ser Ser Ser Phe Val Asp
 180 185 190
 Ser Asp Glu Asp Asp Ser Thr Ser Arg Leu Ser Ser Ser Thr Glu Gln
 195 200 205
 Ser Thr Ser Ser Arg Leu Ile Arg Lys His Lys Arg Arg Arg Arg Lys
 210 215 220

Gln Arg Leu Arg Gln Ala Asp Arg Ala Ser Ser Phe Ser Ser Met Thr
 225 230 235 240
 Asp Ser Thr Met Ser Leu Asn Ile Ile Thr Val Thr Leu Asn Met Glu
 245 250 255
 Arg His His Phe Leu Gly Ile Cys Ile Val Gly Gln Ser Asn Asp Arg
 260 265 270
 Gly Asp Gly Gly Ile Tyr Ile Gly Ser Ile Met Lys Gly Gly Ala Val
 275 280 285
 Ala Ala Asp Gly Arg Ile Glu Pro Gly Asp Met Leu Leu Gln Val Asn
 290 295 300
 Asp Val Asn Phe Glu Asn Met Ser Asn Asp Asp Ala Val Arg Val Leu
 305 310 315 320
 Arg Glu Ile Val Ser Gln Thr Gly Pro Ile Ser Leu Thr Val Ala Lys
 325 330 335
 Cys Trp Asp Pro Thr
 340

<210> 465
 <211> 198
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DVL1 Construct (N)

<400> 465
 Met Ala Glu Thr Lys Ile Ile Tyr His Met Asp Glu Glu Glu Thr Pro
 1 5 10 15
 Tyr Leu Val Lys Leu Pro Val Ala Pro Glu Arg Val Thr Leu Ala Asp
 20 25 30
 Phe Lys Asn Val Leu Ser Asn Arg Pro Val His Ala Tyr Lys Phe Phe
 35 40 45
 Phe Lys Ser Met Asp Gln Asp Phe Gly Val Val Lys Glu Glu Ile Phe
 50 55 60
 Asp Asp Asn Ala Lys Leu Pro Cys Phe Asn Gly Arg Val Val Ser Trp
 65 70 75 80
 Leu Val Leu Val Glu Gly Ala His Ser Asp Ala Gly Ser Gln Gly Thr
 85 90 95
 Asp Ser His Thr Asp Leu Pro Pro Pro Leu Glu Arg Thr Gly Gly Ile
 100 105 110
 Gly Asp Ser Arg Ser Pro Ser Phe Gln Pro Asp Val Ala Ser Ser Arg
 115 120 125
 Asp Gly Met Asp Asn Glu Thr Gly Thr Glu Ser Met Val Ser His Arg
 130 135 140
 Arg Asp Arg Ala Arg Arg Arg Asn Arg Glu Glu Ala Ala Arg Thr Asn
 145 150 155 160
 Gly His Pro Arg Gly Asp Arg Arg Arg Asp Val Gly Leu Pro Pro Asp
 165 170 175
 Ser Ala Ser Thr Ala Leu Ser Ser Glu Leu Glu Ser Ser Ser Phe Val
 180 185 190
 Asp Ser Asp Glu Asp Gly
 195

<210> 466
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DVL1 Construct (P)

<400> 466
 Ser Leu Asn Ile Ile Thr Val Thr Leu Asn Met Glu Arg His His Phe
 1 5 10 15
 Leu Gly Ile Cys Ile Val Gly Gln Ser Asn Asp Arg Gly Asp Gly Gly
 20 25 30
 Ile Tyr Ile Gly Ser Ile Met Lys Gly Gly Ala Val Ala Ala Asp Gly
 35 40 45
 Arg Ile Glu Pro Gly Asp Met Leu Leu Gln Val Asn Asp Val Asn Phe
 50 55 60
 Glu Asn Met Ser Asn Asp Asp Ala Val Arg Val Leu Arg Glu Ile Val
 65 70 75 80
 Ser Gln Thr Gly Pro Ile Ser Leu Thr Val Ala Lys Cys Trp Asp Pro
 85 90 95
 Thr

<210> 467
 <211> 427
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KIAA 0751 Construct (N-J)

<400> 467
 Met Met Tyr Phe Gly Gly His Ser Leu Glu Glu Asp Leu Glu Trp Ser
 1 5 10 15
 Glu Pro Gln Ile Lys Asp Ser Gly Val Asp Thr Cys Ser Ser Thr Thr
 20 25 30
 Leu Asn Glu Glu His Ser His Ser Asp Lys His Pro Val Thr Trp Gln
 35 40 45
 Pro Ser Lys Asp Gly Asp Arg Leu Ile Gly Arg Ile Leu Leu Asn Lys
 50 55 60
 Arg Leu Lys Asp Gly Ser Val Pro Arg Asp Ser Gly Ala Met Leu Gly
 65 70 75 80
 Leu Lys Val Val Gly Gly Lys Met Thr Glu Ser Gly Arg Leu Cys Ala
 85 90 95
 Phe Ile Thr Lys Val Lys Lys Gly Ser Leu Ala Asp Thr Val Gly His
 100 105 110
 Leu Arg Pro Gly Asp Glu Val Leu Glu Trp Asn Gly Arg Leu Leu Gln
 115 120 125
 Gly Ala Thr Phe Glu Glu Val Tyr Asn Ile Ile Leu Glu Ser Lys Pro
 130 135 140
 Glu Pro Gln Val Glu Leu Val Val Ser Arg Pro Ile Gly Asp Ile Pro
 145 150 155 160
 Arg Ile Pro Asp Ser Thr His Ala Gln Leu Glu Ser Ser Ser Ser
 165 170 175
 Phe Glu Ser Gln Lys Met Asp Arg Pro Ser Ile Ser Val Thr Ser Pro
 180 185 190
 Met Ser Pro Gly Met Leu Arg Asp Val Pro Gln Phe Leu Ser Gly Gln
 195 200 205
 Leu Ser Ile Lys Leu Trp Phe Asp Lys Val Gly His Gln Leu Ile Val
 210 215 220
 Thr Ile Leu Gly Ala Lys Asp Leu Pro Ser Arg Glu Asp Gly Arg Pro
 225 230 235 240
 Arg Asn Pro Tyr Val Lys Ile Tyr Phe Leu Pro Asp Arg Ser Asp Lys
 245 250 255
 Asn Lys Arg Arg Thr Lys Thr Val Lys Lys Thr Leu Glu Pro Lys Trp
 260 265 270
 Asn Gln Thr Phe Ile Tyr Ser Pro Val His Arg Arg Glu Phe Arg Glu
 275 280 285

Arg Met Leu Glu Ile Thr Leu Trp Asp Gln Ala Arg Val Arg Glu Glu
 290 295 300
 Glu Ser Glu Phe Leu Gly Glu Ile Leu Ile Glu Leu Glu Thr Ala Leu
 305 310 315 320
 Leu Asp Asp Glu Pro His Trp Tyr Lys Leu Gln Thr His Asp Val Ser
 325 330 335
 Ser Leu Pro Leu Pro His Pro Ser Pro Tyr Met Pro Arg Arg Gln Leu
 340 345 350
 His Gly Glu Ser Pro Thr Arg Arg Leu Gln Arg Ser Lys Arg Ile Ser
 355 360 365
 Asp Ser Glu Val Ser Asp Tyr Asp Cys Asp Asp Gly Ile Gly Val Val
 370 375 380
 Ser Asp Tyr Arg His Asp Gly Arg Asp Leu Gln Ser Ser Thr Leu Ser
 385 390 395 400
 Val Pro Glu Gln Val Met Ser Ser Asn His Cys Ser Pro Ser Gly Ser
 405 410 415
 Pro His Arg Val Asp Val Ile Gly Arg Thr Thr
 420 425

<210> 468
 <211> 92
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KIAA 0751 Construct (P)

<400> 468
 Leu Lys Asp Gly Ser Val Pro Arg Asp Ser Gly Ala Met Leu Gly Leu
 1 5 10 15
 Lys Val Val Gly Gly Lys Met Thr Glu Ser Gly Arg Leu Cys Ala Phe
 20 25 30
 Ile Thr Lys Val Lys Lys Gly Ser Leu Ala Asp Thr Val Gly His Leu
 35 40 45
 Arg Pro Gly Asp Glu Val Leu Glu Trp Asn Gly Arg Leu Leu Gln Gly
 50 55 60
 Ala Thr Phe Glu Glu Val Tyr Asn Ile Ile Leu Glu Ser Lys Pro Glu
 65 70 75 80
 Pro Gln Val Glu Leu Val Val Ser Arg Pro Ile Ala
 85 90

<210> 469
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PAR6 Construct (N-P)

<400> 469
 Met Ala Arg Pro Gln Arg Thr Pro Ala Arg Ser Pro Asp Ser Ile Val
 1 5 10 15
 Glu Val Lys Ser Lys Phe Asp Ala Glu Phe Arg Arg Phe Ala Leu Pro
 20 25 30
 Arg Ala Ser Val Ser Gly Phe Gln Glu Phe Ser Arg Leu Leu Arg Ala
 35 40 45
 Val His Gln Ile Pro Gly Leu Asp Val Leu Leu Gly Tyr Thr Asp Ala
 50 55 60
 His Gly Asp Leu Leu Pro Leu Thr Asn Asp Asp Ser Leu His Arg Ala
 65 70 75 80

Leu Ala Ser Gly Pro Pro Pro Leu Arg Leu Leu Val Gln Lys Arg Glu
 85 90 95
 Ala Asp Ser Ser Gly Leu Ala Phe Ala Ser Asn Ser Leu Gln Arg Arg
 100 105 110
 Lys Lys Gly Leu Leu Leu Arg Pro Val Ala Pro Leu Arg Thr Arg Pro
 115 120 125
 Pro Leu Leu Ile Ser Leu Pro Gln Asp Phe Arg Gln Val Ser Ser Val
 130 135 140
 Ile Asp Val Asp Leu Leu Pro Glu Thr His Arg Arg Val Arg Leu His
 145 150 155 160
 Lys His Gly Ser Asp Arg Pro Leu Gly Phe Tyr Ile Arg Asp Gly Met
 165 170 175
 Ser Val Arg Val Ala Pro Gln Gly Leu Glu Arg Val Pro Gly Ile Phe
 180 185 190
 Ile Ser Arg Leu Val Arg Gly Gly Leu Ala Glu Ser Thr Gly Leu Leu
 195 200 205
 Ala Val Ser Asp Glu Ile Leu Glu Val Asn Gly Ile Glu Val Ala Gly
 210 215 220
 Lys Thr Leu Asp Gln Val Thr Asp Met Met Val Ala Asn Ser His Asn
 225 230 235 240
 Leu Ile Val Thr Val Lys Pro Ala Asn Gln Arg
 245 250

<210> 470
 <211> 146
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PAR6 Construct (N)

<400> 470
 Met Ala Arg Pro Gln Arg Thr Pro Ala Arg Ser Pro Asp Ser Ile Val
 1 5 10 15
 Glu Val Lys Ser Lys Phe Asp Ala Glu Phe Arg Arg Phe Ala Leu Pro
 20 25 30
 Arg Ala Ser Val Ser Gly Phe Gln Glu Phe Ser Arg Leu Leu Arg Ala
 35 40 45
 Val His Gln Ile Pro Gly Leu Asp Val Leu Leu Gly Tyr Thr Asp Ala
 50 55 60
 His Gly Asp Leu Leu Pro Leu Thr Asn Asp Asp Ser Leu His Arg Ala
 65 70 75 80
 Leu Ala Ser Gly Pro Pro Pro Leu Arg Leu Leu Val Gln Lys Arg Glu
 85 90 95
 Ala Asp Ser Ser Gly Leu Ala Phe Ala Ser Asn Ser Leu Gln Arg Arg
 100 105 110
 Lys Lys Gly Leu Leu Leu Arg Pro Val Ala Pro Leu Arg Thr Arg Pro
 115 120 125
 Pro Leu Leu Ile Ser Leu Pro Gln Asp Arg Gln Val Ser Ser Val Ile
 130 135 140
 Asp Val
 145

<210> 471
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PAR6 Construct (P)

<400> 471
 Arg Arg Val Arg Leu His Lys His Gly Ser Asp Arg Pro Leu Gly Phe
 1 5 10 15
 Tyr Ile Arg Asp Gly Met Ser Val Arg Val Ala Pro Gln Gly Leu Glu
 20 25 30
 Arg Val Pro Gly Ile Phe Ile Ser Arg Leu Val Arg Gly Gly Leu Ala
 35 40 45
 Glu Ser Thr Gly Leu Leu Ala Val Ser Asp Glu Ile Leu Glu Val Asn
 50 55 60
 Gly Ile Glu Val Ala Gly Lys Thr Leu Asp Gln Val Thr Asp Met Met
 65 70 75 80
 Val Ala Asn Ser His Asn Leu Ile Val Thr Val Lys Pro Ala Asn Gln
 85 90 95
 Arg

<210> 472
 <211> 442
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PSD95 Construct (N-P3)

<400> 472
 Met Ser Gln Arg Pro Arg Ala Pro Arg Ser Ala Leu Trp Leu Leu Ala
 1 5 10 15
 Pro Pro Leu Leu Arg Trp Ala Pro Pro Leu Leu Thr Val Leu His Ser
 20 25 30
 Asp Leu Phe Gln Ala Leu Leu Asp Ile Leu Asp Tyr Tyr Glu Ala Ser
 35 40 45
 Leu Ser Glu Ser Gln Lys Tyr Arg Tyr Gln Asp Glu Asp Thr Pro Pro
 50 55 60
 Leu Glu His Ser Pro Ala His Leu Pro Asn Gln Ala Asn Ser Pro Pro
 65 70 75 80
 Val Ile Val Asn Thr Asp Thr Leu Glu Ala Pro Gly Tyr Glu Leu Gln
 85 90 95
 Val Asn Gly Thr Glu Gly Glu Met Glu Tyr Glu Glu Ile Thr Leu Glu
 100 105 110
 Arg Gly Asn Ser Gly Leu Gly Phe Ser Ile Ala Gly Gly Thr Asp Asn
 115 120 125
 Pro His Ile Gly Asp Asp Pro Ser Ile Phe Ile Thr Lys Ile Ile Pro
 130 135 140
 Gly Gly Ala Ala Ala Gln Asp Gly Arg Leu Arg Val Asn Asp Ser Ile
 145 150 155 160
 Leu Phe Val Asn Glu Val Asp Val Arg Glu Val Thr His Ser Ala Ala
 165 170 175
 Val Glu Ala Leu Lys Glu Ala Gly Ser Ile Val Arg Leu Tyr Val Met
 180 185 190
 Arg Arg Lys Pro Pro Ala Glu Lys Val Met Glu Ile Lys Leu Ile Lys
 195 200 205
 Gly Pro Lys Gly Leu Gly Phe Ser Ile Ala Gly Gly Val Gly Asn Gln
 210 215 220
 His Ile Pro Gly Asp Asn Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly
 225 230 235 240
 Gly Ala Ala His Lys Asp Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu
 245 250 255
 Ala Val Asn Ser Val Gly Leu Glu Asp Val Met His Glu Asp Ala Val
 260 265 270
 Ala Ala Leu Lys Asn Thr Tyr Asp Val Val Tyr Leu Lys Val Ala Lys
 275 280 285

Pro Ser Asn Ala Tyr Leu Ser Asp Ser Tyr Ala Pro Pro Asp Ile Thr
 290 295 300
 Thr Ser Tyr Ser Gln His Leu Asp Asn Glu Ile Ser His Ser Ser Tyr
 305 310 315 320
 Leu Gly Thr Asp Tyr Pro Thr Ala Met Thr Pro Thr Ser Pro Arg Arg
 325 330 335
 Tyr Ser Pro Val Ala Lys Asp Leu Leu Gly Glu Glu Asp Ile Pro Arg
 340 345 350
 Glu Pro Arg Arg Ile Val Ile His Arg Gly Ser Thr Gly Leu Gly Phe
 355 360 365
 Asn Ile Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe Ile
 370 375 380
 Leu Ala Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly Asp
 385 390 395 400
 Gln Ile Leu Ser Val Asn Gly Val Asp Leu Arg Asn Ala Ser His Glu
 405 410 415
 Gln Ala Ala Ile Ala Leu Lys Asn Ala Gly Gln Thr Val Thr Ile Ile
 420 425 430
 Ala Gln Tyr Lys Pro Glu Glu Tyr Ser Arg
 435 440

<210> 473
 <211> 84
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CASK Construct (P)

<400> 473
 Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile Thr
 1 5 10 15
 Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met His
 20 25 30
 Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu Ile
 35 40 45
 Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln Leu
 50 55 60
 Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile Val
 65 70 75 80
 Pro Ser Tyr Arg

<210> 474
 <211> 294
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MPP2/DLG2 Construct (N-SH3)

<400> 474
 Met Pro Val Ala Ala Thr Asn Ser Glu Thr Ala Met Gln Gln Val Leu
 1 5 10 15
 Asp Asn Leu Gly Ser Leu Pro Ser Ala Thr Gly Ala Ala Glu Leu Asp
 20 25 30
 Leu Ile Phe Leu Arg Gly Ile Met Glu Ser Pro Ile Val Arg Ser Leu
 35 40 45
 Ala Lys Ala His Glu Arg Leu Glu Glu Thr Lys Leu Glu Ala Val Arg
 50 55 60

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Asp Asn Asn Leu Glu Leu Val Gln Glu Ile Leu Arg Asp Leu Ala Gln
65          70          75          80
Leu Ala Glu Gln Ser Ser Thr Ala Ala Glu Leu Ala His Ile Leu Gln
      85          90          95
Glu Pro His Phe Gln Ser Leu Leu Glu Thr His Asp Ser Val Ala Ser
      100        105        110
Lys Thr Tyr Glu Thr Pro Pro Pro Ser Pro Gly Leu Asp Pro Thr Phe
      115        120        125
Ser Asn Gln Pro Val Pro Pro Asp Ala Val Arg Met Val Gly Ile Arg
      130        135        140
Lys Thr Ala Gly Glu His Leu Gly Val Thr Phe Arg Val Glu Gly Gly
145          150        155        160
Glu Leu Val Ile Ala Arg Ile Leu His Gly Gly Met Val Ala Gln Gln
      165        170        175
Gly Leu Leu His Val Gly Asp Ile Ile Lys Glu Val Asn Gly Gln Pro
      180        185        190
Val Gly Ser Asp Pro Arg Ala Leu Gln Glu Leu Leu Arg Asn Ala Ser
      195        200        205
Gly Ser Val Ile Leu Lys Ile Leu Pro Ser Tyr Gln Glu Pro His Leu
      210        215        220
Pro Arg Gln Val Phe Val Lys Cys His Phe Asp Tyr Asp Pro Ala Arg
225          230        235        240
Asp Ser Leu Ile Pro Cys Lys Glu Ala Gly Leu Arg Phe Asn Ala Gly
      245        250        255
Asp Leu Leu Gln Ile Val Asn Gln Asp Asp Ala Asn Trp Trp Gln Ala
      260        265        270
Cys His Val Glu Gly Gly Ser Ala Gly Leu Ile Pro Ser Gln Leu Leu
      275        280        285
Glu Glu Lys Arg Lys Gly
290

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<210> 475
<211> 121
<212> PRT
<213> Artificial Sequence

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<220>
<223> TIP1 Construct (N-C)

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<400> 475
Tyr Ile Pro Gly Gln Pro Val Thr Ala Val Val Gln Arg Val Glu Ile
1      5      10      15
His Lys Leu Arg Gln Gly Glu Asn Leu Ile Leu Gly Phe Ser Ile Gly
      20      25      30
Gly Gly Ile Asp Gln Asp Pro Ser Gln Asn Pro Phe Ser Glu Asp Lys
      35      40      45
Thr Asp Lys Gly Ile Tyr Val Thr Arg Val Ser Glu Gly Gly Pro Ala
      50      55      60
Glu Ile Ala Gly Leu Gln Ser Gly Asp Lys Ile Met Gln Val Asn Gly
65          70          75          80
Trp Asp Met Thr Met Val Thr His Asp Gln Ala Arg Lys Arg Leu Thr
      85          90          95
Lys Arg Ser Glu Glu Val Val Arg Leu Leu Val Thr Arg Gln Ser Leu
      100        105        110
Gln Lys Ala Val Gln Gln Ser Met Leu
      115        120

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<210> 476
<211> 28
<212> DNA
<213> Artificial Sequence

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<220>
 <223> primer 308 DVF (N 128 - N 155)

 <400> 476
 tcggaattcg tcgcgccatg gcggagac 28

 <210> 477
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 311 DVR (N 1004 - N 1032)

 <400> 477
 ggggaattcgg tcccagcact tggccacag 29

 <210> 478
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 344 DVF (N 873 - N 900)

 <400> 478
 ccagaattct caacatcgtc actgtcac 28

 <210> 479
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 345 DVR (N713 - N744)

 <400> 479
 tcggaattcc atcctcgtcc gaggccacaa ag 32

 <210> 480
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 318 KIF (N 1366 - N 1393)

 <400> 480
 agacaattga ggaaatgatg tacttttg 28

 <210> 481
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 319 KIR (N 1830 - N 1857)

 <400> 481
 gaacaattgc aataggcctt gaaactac 28

<210> 482
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 320 KIR (N 2640 -N 2667)

 <400> 482
 accccaattgt agtccttcct ataacatc 28

 <210> 483
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 341 KIF (N 1567 - N 1593)

 <400> 483
 atagaattct aaaagatgga agtgtac 27

 <210> 484
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 322 PAF (N 55 - N 82)

 <400> 484
 cccgaattcg ccatggcccg gccgcagag 29

 <210> 485
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 324 PAR (N 798 - N 825)

 <400> 485
 cgtgaattcg ctggttggcg ggcttgac 28

 <210> 486
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 342 PAF (N 519 - N 548)

 <400> 486
 gaggaattcc gacgggtgcg gctgcacaag 30

 <210> 487
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 343 PAR (N 485 - N 516)

 <400> 487
 gcagaattcc cacgtctatg actgaggaaa c 31

 <210> 488
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 315 PSF (N847 - N876)

 <400> 488
 agagaattca gagatatgtc ccagagacca ag 32

 <210> 489
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 304 PSR (N 2161 - N 2189)

 <400> 489
 cgagaattct gtactcttct ggtttatac 29

 <210> 490
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer 336 CAF (N 1484 - N 1512)

 <400> 490
 ccagaattcg gctggtacag tttcaaaag 29

 <210> 491
 <211> 29
 <212> DNA
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 <220>
 <223> primer 325 CAR (N 1722 - N 1750)

 <400> 491
 actgaattcg gtaacttggc acaatcttg 29

 <210> 492
 <211> 27
 <212> DNA
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 <220>
 <223> primer 305 MF (N 58 - N 84)

 <400> 492
 agagaattca gagcccttgc ctccttc 27

<210> 493
 <211> 28
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 <220>
 <223> primer 306 MR (N 798 - N 825)

 <400> 493
 tgagaattcc tttccgcttc tcctccag 28

 <210> 494
 <211> 21
 <212> DNA
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 <220>
 <223> primer 1318 TIP R3-1 (N 336 - N 356)

 <400> 494
 cagtccatgc tgtcggatcc g 21

 <210> 495
 <211> 21
 <212> DNA
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 <220>
 <223> primer 1317 TIP R5-1

 <400> 495
 gtcggaattc cctacatccc g 21

 <210> 496
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> PDZ consensus

 <400> 496
 Glu Thr Gln Val
 1

 <210> 497
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV57 E6 PL motif

 <400> 497
 Arg Thr Ser His
 1

 <210> 498
 <211> 4
 <212> PRT
 <213> Artificial Sequence

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    <220>
    <223> HPV2a E6 PL motif

    <400> 498
Arg Thr Leu His
1

    <210> 499
    <211> 4
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> HPV63 E6 PL motif

    <400> 499
Leu Tyr Ile Ile
1

    <210> 500
    <211> 4
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> HPV77 E6 PL motif

    <400> 500
Gln Ser Arg Gln
1

    <210> 501
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    <212> PRT
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    <220>
    <223> HPV80 E6 PL motif

    <400> 501
Gly Ser Ile Glu
1

    <210> 502
    <211> 10
    <212> PRT
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    <220>
    <223> HPV61 E6 C-terminal

    <400> 502
Thr Gly Pro Cys Thr Ala Arg Trp Gln Pro
1          5          10

    <210> 503
    <211> 12
    <212> PRT
    <213> Artificial Sequence

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<220>
 <223> HPV60 E6 C-terminal

 <400> 503
 Arg Gln Arg Ser Tyr Cys Arg Asn Cys Ile Glu Lys
 1 5 10

 <210> 504
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV55 E6 C-terminal

 <400> 504
 Cys Trp Thr Ser Cys Met Glu Thr Ile Leu Pro
 1 5 10

 <210> 505
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV50 E6 C-terminal

 <400> 505
 Cys Cys Arg Asn Cys Tyr Glu His Glu Gly
 1 5 10

 <210> 506
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV48 E6 C-terminal

 <400> 506
 Cys Arg Asn Cys Ile Ser His Glu Gly Arg
 1 5 10

 <210> 507
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV44 E6 C-terminal

 <400> 507
 Cys Phe His Cys Trp Thr Ser Cys Met Glu Thr Ile Leu Pro
 1 5 10

 <210> 508
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV38 E6 C-terminal

 <400> 508
 Gly Asn Trp Lys Gly Arg Cys Arg His Cys Lys Ala Ile Glu
 1 5 10

 <210> 509
 <211> 12
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV37 E6 C-terminal

 <400> 509
 Trp Lys Gly Leu Cys Arg His Cys Gly Ser Ile Gly
 1 5 10

 <210> 510
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV66 E6 C-terminal

 <400> 510
 Thr Gly Ser Cys Leu Gln Cys Trp Arg His Thr Ser Arg Gln Ala Thr
 1 5 10 15
 Glu Ser Thr Val
 20

 <210> 511
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV57 E6 C-terminal

 <400> 511
 Arg Cys Met Asn Cys Ala Pro Arg Cys Met Glu Asn Ala Pro Ala Leu
 1 5 10 15
 Arg Thr Ser His
 20

 <210> 512
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV2a E6 C-terminal

 <400> 512
 His Cys Met Asn Cys Gly Ser Ser Cys Thr Ala Thr Asp Pro Ala Ser
 1 5 10 15
 Arg Thr Leu His
 20

<210> 513
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV16 E6 C-terminal

 <400> 513
 Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser Arg Thr Arg Arg
 1 5 10 15
 Glu Thr Gln Leu
 20

 <210> 514
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV18 E6 C-terminal

 <400> 514
 His Ser Cys Cys Asn Arg Ala Arg Gln Glu Arg Leu Gln Arg Arg Arg
 1 5 10 15
 Glu Thr Gln Val
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 <210> 515
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV31 E6 C-terminal

 <400> 515
 Gly Arg Trp Thr Gly Arg Cys Ile Ala Cys Trp Arg Arg Pro Arg Thr
 1 5 10 15
 Glu Thr Gln Val
 20

 <210> 516
 <211> 21
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV33 E6 C-terminal

 <400> 516
 Cys Ala Ala Cys Trp Arg Ser Ala Arg Arg Arg Arg Leu Gln Arg Arg
 1 5 10 15
 Arg Glu Thr Ala Leu
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 <210> 517
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV51 E6 C-terminal

 <400> 517
 Cys Ala Asn Cys Trp Gln Arg Thr Arg Gln Arg Arg Leu Gln Arg Arg
 1 5 10 15
 Asn Glu Thr Gln Val
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 <210> 518
 <211> 21
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV52 E6 C-terminal

 <400> 518
 Cys Ser Glu Cys Trp Arg Pro Thr Arg Arg Pro Arg Leu Gln Arg Arg
 1 5 10 15
 Arg Val Thr Gln Val
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 <210> 519
 <211> 21
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV58 E6 C-terminal

 <400> 519
 Cys Ala Val Cys Trp Arg Pro Ala Arg Arg Arg Arg Leu Gln Arg Arg
 1 5 10 15
 Arg Gln Thr Gln Val
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 <210> 520
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV70 E6 C-terminal

 <400> 520
 Arg His Cys Trp Thr Ser Asn Arg Glu Asp Arg Arg Arg Ile Arg Arg
 1 5 10 15
 Glu Thr Gln Val
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 <210> 521
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV63 E6 C-terminal

<400> 521
 Val His Lys Val Arg Asn Lys Phe Lys Ala Lys Cys Ser Leu Cys Arg
 1 5 10 15
 Leu Tyr Ile Ile
 20

<210> 522
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV77 E6 C-terminal

<400> 522
 Gly His Trp Arg Gly Ser Cys Leu His Cys Trp Ser Arg Cys Met Gly
 1 5 10 15
 Gln Ser Arg Gln
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<210> 523
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV80 E6 C-terminal

<400> 523
 Gln Phe His Lys Val Arg Arg Asn Trp Lys Gly Leu Cys Arg His Cys
 1 5 10 15
 Gly Ser Ile Glu
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<210> 524
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV21 E6 C-terminal

<400> 524
 Trp Lys Gly Ile Cys Arg Leu Cys Lys His Phe Gln
 1 5 10

<210> 525
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV11 E6 C-terminal

<400> 525
 Trp Lys Gly Arg Cys Leu His Cys Trp Thr Thr Cys Met Glu Asp Leu
 1 5 10 15
 Leu Pro

<210> 526
 <211> 15
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV36 E6 C-terminal

 <400> 526
 Trp Lys Gly Ile Cys Arg Gln Cys Lys His Phe Tyr Asn Asp Trp
 1 5 10 15

 <210> 527
 <211> 18
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV29 E6 C-terminal

 <400> 527
 Trp Arg Gly Ser Cys Leu Tyr Cys Trp Ser Arg Cys Met Gly Gln Ser
 1 5 10 15
 Pro Arg

 <210> 528
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV28 E6 C-terminal

 <400> 528
 Cys Gln Tyr Cys Trp Leu Arg Cys Thr Val Arg Ile Pro Gln
 1 5 10

 <210> 529
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV24 E6 C-terminal

 <400> 529
 Lys Val Arg Arg Gly Trp Lys Gly Leu Cys Arg Gln Cys Lys Gln Ile
 1 5 10 15

 <210> 530
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV22 E6 C-terminal

 <400> 530
 Val Arg Asp His Trp Lys Gly Arg Cys Arg His Cys Lys Ala Ile Glu
 1 5 10 15

<210> 531
 <211> 18
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV21 E6 C-terminal

 <400> 531
 His Lys Val Arg Gly Ser Trp Lys Gly Ile Cys Arg Leu Cys Lys His
 1 5 10 15
 Phe Gln

<210> 532
 <211> 19
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV20 E6 C-terminal

 <400> 532
 Phe Tyr Leu Val Arg Gly Ser Trp Lys Gly Ile Cys Arg Leu Cys Lys
 1 5 10 15
 His Phe Gln

<210> 533
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV4 E6 C-terminal

 <400> 533
 Thr Cys Tyr Leu Ile Arg Gly Leu Trp Arg Gly Tyr Cys Arg Asn Cys
 1 5 10 15
 Ile Arg Lys Gln
 20

<210> 534
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV54 E6 C-terminal

 <400> 534
 Arg Arg Phe His Cys Val Arg Gly Tyr Trp Lys Gly Arg Cys Leu His
 1 5 10 15
 Cys Trp Lys Pro
 20

<210> 535
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HPV5B E6 C-terminal

 <400> 535
 Lys Val Arg Asn Ala Trp Lys Gly Ile Cys Arg Gln Cys Lys His Phe
 1 5 10 15
 Tyr His Asp Trp
 20

 <210> 536
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV74 E6 C-terminal

 <400> 536
 Asn Thr Trp Lys Gly Arg Cys Phe His Cys Trp Thr Thr Cys Met Glu
 1 5 10 15
 Asn Ile Leu Pro
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 <210> 537
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV75 and HPV76 E6 C-terminal

 <400> 537
 Glu Phe His Lys Val Arg Asn Arg Trp Lys Gly Val Cys Arg His Cys
 1 5 10 15
 Arg Val Ile Glu
 20

 <210> 538
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV47 E6 C-terminal

 <400> 538
 Lys Val Arg Asn Ala Trp Lys Gly Val Cys Arg Gln Cys Lys His Phe
 1 5 10 15
 Tyr Asn Asp Trp
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 <210> 539
 <211> 20
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> HPV65 E6 C-terminal

<400> 539
 Ala Cys Tyr Leu Ile Arg Gly Leu Trp Arg Gly Tyr Cys Arg Asn Cys
 1 5 10 15
 Ile Arg Lys Gln
 20

<210> 540
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence unique to vector pDsRED1-N1(+ATG)

<400> 540
 attgccacca tgggaattct ggatccggga gat

33

<210> 541
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> flexible polylinker

<400> 541
 Gly Gly Gly Gly Ser
 1 5

<210> 542
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> linker

<400> 542
 Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
 1 5 10

<210> 543
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> linker

<400> 543
 Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
 1 5 10 15
 Leu Asp